1812

INPUT SET: S21923.raw

┌───┐
│ **This Raw Listing contains the General**   │
│ **Information Section and up to the first 5 pages.** │
└───┘

#5 |ATR.
02|04|98

ENTERED

```
 1                          SEQUENCE LISTING
 2
 3   (1)     General Information:
 4
 5      (i) APPLICANTS: WEI, YING-FEI
 6                      KREIDER, BRENT
 7                      ROSEN, CRAIG
 8
 9     (ii) TITLE OF INVENTION: CHEMOKINE BETA 15
10
11    (iii) NUMBER OF SEQUENCES: 9
12
13     (iv) CORRESPONDENCE ADDRESS:
14             (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
15             (B) STREET: 1100 NEW YORK AVENUE, SUITE 600
16             (C) CITY: WASHINGTON
17             (D) STATE: D.C.
18             (E) COUNTRY: US
19             (F) ZIP: 20005-3934
20
21      (v) COMPUTER READABLE FORM:
22             (A) MEDIUM TYPE: Floppy disk
23             (B) COMPUTER: IBM PC compatible
24             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25             (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27     (vi) CURRENT APPLICATION DATA:
28             (A) APPLICATION NUMBER: (To Be Assigned)
29             (B) FILING DATE: HEREWITH
30             (C) CLASSIFICATION:
31
32    (vii) PRIOR APPLICATION DATA:
33             (A) APPLICATION NUMBER: 60/019,837
34             (B) FILING DATE: 17-JUN-1996
35
36   (viii) ATTORNEY/AGENT INFORMATION:
37             (A) NAME: Steffe, Eric K.
38             (B) REGISTRATION NUMBER: 36,688
39             (C) REFERENCE/DOCKET NUMBER: 1488.0420001
40
41     (ix) TELECOMMUNICATION INFORMATION:
42             (A) TELEPHONE: 202-371-2600
43             (B) TELEFAX: 202-371-2540
44
45   (2) INFORMATION FOR SEQ ID NO:1:
46
```

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/874,460*

DATE: 12/04/97
TIME: 15:39:10

INPUT SET: S21923.raw

```
47          (i) SEQUENCE CHARACTERISTICS:
48              (A) LENGTH: 989 base pairs
49              (B) TYPE: nucleic acid
50              (C) STRANDEDNESS: single
51              (D) TOPOLOGY: linear
52
53         (ii) MOLECULE TYPE: DNA (genomic)
54
55
56         (ix) FEATURE:
57              (A) NAME/KEY: CDS
58              (B) LOCATION: 88..534
59
60         (ix) FEATURE:
61              (A) NAME/KEY: sig_peptide
62              (B) LOCATION: 88..147
63
64         (ix) FEATURE:
65              (A) NAME/KEY: mat_peptide
66              (B) LOCATION: 148..534
67
68
69         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
70
71  CCGGCGGGCA TCAGCTCCCT TGACCCAGTG GATATCGGTG GCCCCGTTAT TCGTCCAGGT     60
72
73  GCCCAGGGAG GAGGACCCGC CTGCAGC ATG AAC CTG TGG CTC CTG GCC TGC       111
74                               Met Asn Leu Trp Leu Leu Ala Cys
75                               -20             -15
76
77  CTG GTG GCC GGC TTC CTG GGA GCC TGG GCC CCC GCT GTC CAC ACC CAA    159
78  Leu Val Ala Gly Phe Leu Gly Ala Trp Ala Pro Ala Val His Thr Gln
79          -10             -5           .  1
80
81  GGT GTC TTT GAG GAC TGC TGC CTG GCC TAC CAC TAC CCC ATT GGG TGG    207
82  Gly Val Phe Glu Asp Cys Cys Leu Ala Tyr His Tyr Pro Ile Gly Trp
83   5               10              15                  20
84
85  GCT GTG CTC CGG CGC GCC TGG ACT TAC CGG ATC CAG GAG GTG AGC GGG    255
86  Ala Val Leu Arg Arg Ala Trp Thr Tyr Arg Ile Gln Glu Val Ser Gly
87          25              30                  35
88
89  AGC TGC AAT CTG CCT GCT GCG ATA TTC TAC CTC CCC AAG AGA CAC AGG    303
90  Ser Cys Asn Leu Pro Ala Ala Ile Phe Tyr Leu Pro Lys Arg His Arg
91          40              45                  50
92
93  AAG GTG TGT GGG AAC CCC AAA AGC AGG GAG GTG CAG AGA GCC ATG AAG    351
94  Lys Val Cys Gly Asn Pro Lys Ser Arg Glu Val Gln Arg Ala Met Lys
95          55              60                  65
96
97  CTC CTG GAT GCT CGA AAT AAG GTT TTT GCA AAG CTC CAC CAC AAC ACG    399
98  Leu Leu Asp Ala Arg Asn Lys Val Phe Ala Lys Leu His His Asn Thr
99          70              75                  80
```

INPUT SET: S21923.raw

```
100
101    CAG ACC TTC CAA GGC CCT CAT GCT GTA AAG AAG TTG AGT TCT GGA AAC        447
102    Gln Thr Phe Gln Gly Pro His Ala Val Lys Lys Leu Ser Ser Gly Asn
103     85              90          Val          95                100
104
105    TCC AAG TTA TCA TCG TCC AAG TTT AGC AAT CCC ATC AGC AGC AGC AAG        495
106    Ser Lys Leu Ser Ser Ser Lys Phe Ser Asn Pro Ile Ser Ser Ser Lys
107                105              110                  115
108
109    AGG AAT GTC TCC CTC CTG ATA TCA GCT AAT TCA GGA CTG TGAGCCGGCT        544
110    Arg Asn Val Ser Leu Leu Ile Ser Ala Asn Ser Gly Leu
111                120                  125
112
113    CATTTCTGGG CTCCATCGGC ACAGGAGGGC CGGATCTTTC TCCGATAAAA CCGTCGCCCT      604
114
115    ACAGACCCAG CTGTCCCCAC GCCTCTGTCT TTTGGGTCAA GTCTTAATCC CTGCACCTGA      664
116
117    GTTGGTCCTC CCTCTGCACC CCCACCACCT CCTGCCCGTC TGGCAACTGG AAAGAGGGAG      724
118
119    TTGGCCTGAT TTTAAGCCTT TTGCCGCTCC GGGGACCAGC AGCAATCCTG GGCAGCCAGT      784
120
121    GGCTCTTGTA GAGAAGACTT AGGATACCTC TCTCACTTTC TGTTTCTTGC CGTCCACCCC      844
122
123    GGGCCATGCC AGTGTGTCCC TCTGGGTCCC TCCAAAACTC TGGTCAGTTC AAGGATGCCC      904
124
125    CTCCCAGGCT ATGCTTTTCT ATAACTTTTA AATAAACCTT GGGGGGTGAT GGAGTCAAAA      964
126
127    AAAAAAAAAA AAAAAAAAAA AAAAA                                           989
128
129
130    (2) INFORMATION FOR SEQ ID NO:2:
131
132         (i) SEQUENCE CHARACTERISTICS:
133              (A) LENGTH: 149 amino acids
134              (B) TYPE: amino acid
135              (D) TOPOLOGY: linear
136
137         (ii) MOLECULE TYPE: protein
138
139         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
140
141    Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala
142    -20              -15              -10                      -5
143
144    Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu
145                  1               5                   10
146
147    Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr
148            15                  20                  25
149
150    Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile
151        30                  35                  40
152
```

PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/874,460*

DATE: 12/04/97
TIME: 15:39:17

INPUT SET: S21923.raw

```
153   Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser
154   45              50              55                      60
155
156
157   Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val
158               65              70                      75
159
160   Phe Ala Lys Leu His His Asn Thr Gln Thr Phe Gln Gly Pro His Ala
161               80              85                      90
162
163   Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys Phe
164           95              100                     105
165
166   Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile Ser
167       110                 115                 120
168
169   Ala Asn Ser Gly Leu
170   125
171
172   (2) INFORMATION FOR SEQ ID NO:3:
173
174       (i) SEQUENCE CHARACTERISTICS:
175           (A) LENGTH: 95 amino acids
176           (B) TYPE: amino acid
177           (C) STRANDEDNESS: single
178           (D) TOPOLOGY: linear
179
180      (ii) MOLECULE TYPE: protein
181
182
183
184
185      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
186
187       Ala Thr Glu Thr Lys Glu Val Gln Ser Ser Leu Lys Ala Gln Gln Gly
188       1               5               10                  15
189
190       Leu Glu Ile Glu Met Phe His Met Gly Phe Gln Asp Ser Ser Asp Cys
191                   20              25                  30
192
193       Cys Leu Ser Tyr Asn Ser Arg Ile Gln Cys Ser Arg Phe Ile Gly Tyr
194               35              40                  45
195
196       Phe Pro Ile Ser Gly Gly Cys Thr Arg Pro Gly Ile Ile Phe Ile Ser
197           50              55                  60
198
199       Lys Arg Gly Phe Gln Val Cys Ala Asn Pro Ser Asp Arg Arg Val Gln
200       65              70                  75                      80
201
202       Arg Cys Arg Leu Glu Gln Asn Ser Gln Pro Arg Thr Tyr Lys Gln
203               85              90                  95
204
205   (2) INFORMATION FOR SEQ ID NO:4:
```

```
206
207        (i) SEQUENCE CHARACTERISTICS:
208            (A) LENGTH: 27 base pairs
209            (B) TYPE: nucleic acid
210            (C) STRANDEDNESS: single
211            (D) TOPOLOGY: linear
212
213       (ii) MOLECULE TYPE: DNA (genomic)
214
215
216
217
218       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
219
220   GCCGTCGACG TCCACACCCA AGGTGTC                                27
221
222   (2) INFORMATION FOR SEQ ID NO:5:
223
224        (i) SEQUENCE CHARACTERISTICS:
225            (A) LENGTH: 30 base pairs
226            (B) TYPE: nucleic acid
227            (C) STRANDEDNESS: single
228            (D) TOPOLOGY: linear
229
230       (ii) MOLECULE TYPE: DNA (genomic)
231
232
233
234
235       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
236
237   GCCTCTAGAG GAGCCCAGAA ATGAGCCGGC                             30
238
239   (2) INFORMATION FOR SEQ ID NO:6:
240
241        (i) SEQUENCE CHARACTERISTICS:
242            (A) LENGTH: 36 base pairs
243            (B) TYPE: nucleic acid
244            (C) STRANDEDNESS: single
245            (D) TOPOLOGY: linear
246
247       (ii) MOLECULE TYPE: DNA (genomic)
248
249
250
251
252       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
253
254   GCCTCTAGAG CCATCATGAA CCTGTGGCTC CTGGCC                      36
255
256   (2) INFORMATION FOR SEQ ID NO:7:
257
258        (i) SEQUENCE CHARACTERISTICS:
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/874,460*

INPUT SET: S21923.raw

Line	Error	Original Text
28	Wrong application Serial Number	(A) APPLICATION NUMBER: (To Be Assigned)